

☐ 1: Immunol Invest. 2002 Aug-Nov;31(3-4):247-62.

[Links](#)

Cross reaction of tetanus and botulinum neurotoxins A and B and the boosting effect of botulinum neurotoxins A and B on a primary anti-tetanus antibody response.

Dolimbek BZ, Jankovic J, Atassi MZ.

Department of Biochemistry and Molecular Biology, Baylor College of Medicine, Houston, Texas, USA.

The present studies were carried out in order to investigate the cross-reaction of botulinum neurotoxins (BoNTs) with human and mouse antibodies against tetanus neurotoxin (TeNT) and determine whether injection of BoNT into a host that has been primed with TeNT would result in boosting of the response to the injected BoNT. Human antisera against TeNT obtained from 9 individuals were found to exhibit substantial cross-reaction with BoNTs A and B. We prepared antibodies (Abs) against inactivated tetanus neurotoxin (TeNT) in outbred mice and determined the binding of these Abs to active TeNT and active botulinum neurotoxins (BoNTs) A and B. Blood samples were collected before immunization (day 0) and on days 42, 82 and 125 after the first injection. The reactions of these sera with the immunizing antigen (inactivated TeNT), active TeNT, active BoNT/A and active BoNT/B were determined. At a fixed dilution (1:62.5 v/v), the sera contained high levels of Abs that reacted with TeNT and also with BoNTs A and B. Throughout the test period (up through day 125) and at different dilutions the cross-reactions of the antisera with BoNT/B were almost twice those with BoNT/A. The reactions of the antisera with the immunizing antigen (inactive TeNT) or with active TeNT were essentially equal throughout the dilution range tested (1:16-1:500 v/v). To determine whether injection of BoNT/A or B into a host that had been primed with TeNT resulted in boosting of the response to the priming antigen (TeNT) as well as BoNT/A or B, mice were primed with TeNT and boosted 21 days later with TeNT, BoNT/A or BoNT/B. Appropriate controls were also employed. Blood samples were collected prior to TeNT priming (day -1) and on days 21, 32, 46 and 67 after priming. In TeNT-primed mice, BoNTs A or B boosted the anti-TeNT Ab responses slightly but had no significant boosting effect on the Ab populations that bind to BoNTs A or B. It is concluded that while Abs against TeNT cross react with BoNTs and the cross reaction with BoNT/B is almost double that of BoNT/A, injection of BoNTs A or B in the presence of a prior active immunity against TeNT is not very likely to make the host mount an Ab response against the injected BoNT.

PMID: 12472183 [PubMed - indexed for MEDLINE]



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Review: 0



☐ 1: [Protein J.](#) 2004 Jan;23(1):39-52.

[Links](#)

Mapping of the antibody-binding regions on the HN-domain (residues 449-859) of botulinum neurotoxin A with antitoxin antibodies from four host species. Full profile of the continuous antigenic regions of the H-chain of botulinum neurotoxin A.

Atassi MZ, Dolimbek BZ.

Verna and Marrs McLean Department of Biochemistry and Molecular Biology, Baylor College of Medicine, Houston, Texas, USA.
matassi@bcm.tmc.edu

Previously, we mapped the antibody (Ab) and T-cell recognition regions on the HC domain (residues 855-1296) of the 848-residue heavy (H) chain of botulinum neurotoxin A (BoNT/A). We have mapped here the HN-domain (residues 449-859) regions that bind protective anti-BoNT/A Abs raised in four different species. We synthesized, purified, and characterized 29 19-residue peptides that spanned the entire HN and overlapped consecutively by 5 residues, and also region L218-231 around the L-chain's substrate-binding site. Human, horse, mouse, and chicken anti-BoNT/A Abs did not bind to the L-peptide but recognized similar HN regions within peptides 519-537/533-551/547-565/561-579 (with slight left- or right-shifts), 743-761, 785-803, and 813-831/827-845 overlap. Recognition of other peptides that bound lower Ab levels showed similarities and also some differences. Peptide 463-481, strongly immunodominant with horse antisera, did not bind human, mouse, and chicken Abs. However, peptide 449-467 bound Abs in these three antisera, and the region may have shifted to the right (peptide 463-481) with horse Abs. The overlap 659-677/673-691 reacted strongly with human Abs whereas with mouse and chicken antisera, only peptide 673-691 showed low reactivity. Horse antisera had no detectable Ab binding to region(s) 659-691. The Ab-recognition regions on the H chain occupy surface locations in BoNT/A three-dimensional structure, but the great part of the surface is not immunogenic. Regions recognized by the protective antisera of the four different species are prime candidates for inclusion in synthetic vaccine designs.

PMID: 15115181 [PubMed - indexed for MEDLINE]

Related Links

Mapping of the antibody and T cell recognition profiles of the HN domain (residues 449-859) of the heavy chain of botulinum neurotoxin A in two high-responder mouse strains. [Immunol Invest. 2005]

Mapping of the antibody-binding regions on botulinum neurotoxin H-chain domain 855-1296 with antitoxin antibodies from three host species. [J Protein Chem. 1996]

Localization of the regions on the C-terminal domain of the heavy chain of botulinum A recognized by T lymphocytes and by antibodies after immunization of mice with pentavalent toxin. [Immunol Invest. 1997]

Submolecular recognition profiles in two mouse strains of non-protective and protective antibodies against botulinum neurotoxin A. [Immunol. 2005]

Mapping of the synaptosome-binding regions on the heavy chain of botulinum neurotoxin A by synthetic overlapping peptides encompassing the entire chain. [Protein J. 2004]

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Oct 24 2006 07:33:51

P04958
TETX_CLOTE

Tetanus toxin precursor (EC 3.4.24.68) (Tentoxylisin)
[Contains:
Tetanus toxin light chain (Tetanus toxin chain L);
Tetanus toxin heavy chain (Tetanus toxin chain H)] [tetX]
[Clostridium tetani]

Score = 1638 bits (4242), Expect = 0.0
Identities = 823/864 (95%), Positives = 823/864 (95%)

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LYNRTASLTDLGGELCIKIKNEDLTfIAEKNSFSEEPFQDEIVSYNTKNKPLNFN
Sbjct: 451 LYNRTASLTDLGGELCIKIKNEDLTfIAEKNSFSEEPFQDEIVSYNTKNKPLNFN

Query: 61 IIVDYNLQSKITLPNDRTPVTKGIPYAPEYKSNAASTIEIHNIDDNTIYQYLYA
IIVDYNLQSKITLPNDRTPVTKGIPYAPEYKSNAASTIEIHNIDDNTIYQYLYA
Sbjct: 511 IIVDYNLQSKITLPNDRTPVTKGIPYAPEYKSNAASTIEIHNIDDNTIYQYLYA

Query: 121 TLQRITMTNSVDDALINSTKIYSYFSPVISKVNQGAQGILFLQWVRDIIDDFtNE
TLQRITMTNSVDDALINSTKIYSYFSPVISKVNQGAQGILFLQWVRDIIDDFtNE
Sbjct: 571 TLQRITMTNSVDDALINSTKIYSYFSPVISKVNQGAQGILFLQWVRDIIDDFtNE

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TIDKISDVSTIVPYIGPALNIVKQGYEGNFIGALETtGVVLLLEYIPEITLPVIA
Sbjct: 631 TIDKISDVSTIVPYIGPALNIVKQGYEGNFIGALETtGVVLLLEYIPEITLPVIA

Query: 241 ESSTQKEKIIKTIDNFLEKRYEKWIEVYKLVKAKWLGTvNTQFQKRSYQMYRSLE
ESSTQKEKIIKTIDNFLEKRYEKWIEVYKLVKAKWLGTvNTQFQKRSYQMYRSLE
Sbjct: 691 ESSTQKEKIIKTIDNFLEKRYEKWIEVYKLVKAKWLGTvNTQFQKRSYQMYRSLE

Query: 301 XXXXXXXXXXXXSGPDKEQIADEIXXXXXXXXXXXXXXXXXMININIFMRESSRSFLV
SGPDKEQIADEI MININIFMRESSRSFLV
Sbjct: 751 IKKIIDYEYKIYSGPDKEQIADEINNlKNKLEEKANKAMININIFMRESSRSFLV

Query: 361 EAKKQLLEFDTQSKNlMQYIKANSKFIGITELKKLESKINKVFSTPIPFsYSKN
EAKKQLLEFDTQSKNlMQYIKANSKFIGITELKKLESKINKVFSTPIPFsYSKN
Sbjct: 811 EAKKQLLEFDTQSKNlMQYIKANSKFIGITELKKLESKINKVFSTPIPFsYSKN

Query: 421 DNEEDIDVILKKSTXXXXXXXXXXXXXXXXXGFNSSVITYPDaQLVPGINGKAIHLV
DNEEDIDVILKKST GFNSSVITYPDaQLVPGINGKAIHLV
Sbjct: 871 DNEEDIDVILKKSTIlNLdINNDIISDISGFNSSVITYPDaQLVPGINGKAIHLV

Query: 481 EVIVHKAMDIEYNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISSMKKHSLS
EVIVHKAMDIEYNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISSMKKHSLS
Sbjct: 931 EVIVHKAMDIEYNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISSMKKHSLS

Query: 541 SVSLKGNNLIWTLKDSAGEVRQITFRDLpDKFNAYLANKWVFITITNDRLSSANL
SVSLKGNNLIWTLKDSAGEVRQITFRDLpDKFNAYLANKWVFITITNDRLSSANL
Sbjct: 991 SVSLKGNNLIWTLKDSAGEVRQITFRDLpDKFNAYLANKWVFITITNDRLSSANL

Query: 601 LMGSAEITGLGAIREDDNNITLKLDRCNNNNQYVVSIDKFRI FCKALNPKEIEKLYT
LMGSAEITGLGAIREDDNNITLKLDRCNNNNQYVVSIDKFRI FCKALNPKEIEKLYT
Sbjct: 1051 LMGSAEITGLGAIREDDNNITLKLDRCNNNNQYVVSIDKFRI FCKALNPKEIEKLYT

Query: 661 TFLRDFWGNPLRYDTEYYLIPVASSSKDVQLKNITDYMyltnapsyTNGKLNIYY
TFLRDFWGNPLRYDTEYYLIPVASSSKDVQLKNITDYMyltnapsyTNGKLNIYY
Sbjct: 1111 TFLRDFWGNPLRYDTEYYLIPVASSSKDVQLKNITDYMyltnapsyTNGKLNIYY

Query: 721 GLKFIIKRYTPNNEIDSFVKSGDFIKLYVSYNNNEHIVGYPKDGNafnnLDRI LR
GLKFIIKRYTPNNEIDSFVKSGDFIKLYVSYNNNEHIVGYPKDGNafnnLDRI LR
Sbjct: 1171 GLKFIIKRYTPNNEIDSFVKSGDFIKLYVSYNNNEHIVGYPKDGNafnnLDRI LR

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PGIPLYKKMEAVKLRDLKTYSVQLKLYDDKNASLGLVGTHNGQIGNDPNRDILIA
Sbjct: 1231 PGIPLYKKMEAVKLRDLKTYSVQLKLYDDKNASLGLVGTHNGQIGNDPNRDILIA

Query: 841 NHLKDKILGCDWYFVPTDEGWTND 864
NHLKDKILGCDWYFVPTDEGWTND
Sbjct: 1291 NHLKDKILGCDWYFVPTDEGWTND 1314

Protein J. 2004 Nov;23(8):539-52.

[Links](#)

Mapping of the synaptosome-binding regions on the heavy chain of botulinum neurotoxin A by synthetic overlapping peptides encompassing the entire chain.

Maruta T, Dolimbek BZ, Aoki KR, Steward LE, Atassi MZ.

Department of Biochemistry and Molecular Biology, Baylor College of Medicine, Houston, Texas 77030, USA.

The purpose of this work was to map, on the heavy (H) chain of botulinum neurotoxin A (BoNT/A), the regions that bind to mouse brain synaptosomes (snps). We prepared 60 synthetic overlapping peptides that had uniform size and overlaps and encompassed the entire H chain (residues 499 to 1296) of BoNT/A. The ability of each peptide to inhibit the binding of 125I-labeled BoNT/A to mouse brain snps was studied. The binding of 125I-labeled BoNT/A to mouse brain snps was completely inhibited by free unlabeled BoNT/A, but not by unrelated proteins, indicating that the binding of BoNT/A to mouse brain snps was a specific event. Inhibition studies with the individual peptides showed that, on the H(N) domain, inhibitory activities greater than 10% were exhibited, in decreasing order, by peptides 799-817, 659-677, 729-747, 533-551, 701-719, and 757-775. Lower inhibitory activities (between 5.6% and 8.7%) were exhibited by five other peptides, 463-481, 505-523, 519-537, 603-621 and 645-663. The remaining 18 H(N) peptides had little or no inhibitory activity. In the H(C) domain, peptides 1065-1083, 1163-1181 and 1275-1296 had the highest inhibitory activities (between 25% and 29%), followed (10-12% inhibitory activity) by peptides 1107-1125, 1191-1209 and 1233-1251. Two other peptides, 1079-1097 and 1177-1195, had very low (5.8% and 4.9%) inhibitory activities. The remaining 23 H(C) peptides had no inhibitory activity. Inhibition with mixtures of equimolar quantities of the most active 6 peptides of HN, 5 of H(C) or all 11 of H(N) and H(C) revealed that the peptides contain independent non-competing binding regions. Comparison of the locations of the snp-binding regions on the H-subunit with the regions that bind blocking mouse anti-BoNT/A Abs helped explain the protecting ability of these Abs. In the three-dimensional structure of BoNT/A, the snp-binding regions that completely coincide or significantly overlap with the antigenic regions occupy surface locations and most of them reside in the last half of the H(C) domain. But some of the regions reside in the HN domain and might play a role in the translocation event.

PMID: 15648976 [PubMed - indexed for MEDLINE]

CLUSTAL FORMAT for T-COFFEE Version_1.37, CPU=0.00 sec, SCORE=16750, Nseq=2, Len=134

```
unk|VIRT3669|Blast_submission -PITINNFRYSDPVNNDTIIMMEPPYCKGLDIYYKAFKITDRIWIVPERYEFG  
tr|Q7B8V4|Q7B8V4_CLOBO MPFVNKQFNYPKDPVNGVDIAYIKIPNA-GQMGPVKAFKIHNKIWVIPERDTFT  
*:..:::*.*.....*::*.*****:::***:*****
```

```
unk|VIRT3669|Blast_submission      NPPSSLIEGASEYYDPNYLRTDSDKDRFLQTMVKLFNRIKNNVAGEALLDKII
tr|Q7B8V4|Q7B8V4_CLOBO             NPPPEAKQVPVSYDYDSTYLSTDNEKDNYLKGVTCLKFERIYSTDLGRMLLTSIV
***. . . : . . . ****. ** ** . : ** . : : . : . : ****. : ** . . . * . ** . * :
```

```
unk|VIRT3669|Blast_submission      NSYLLDKFDTSNSVSFNLLQDPGSGATTKSAMLTLNLIIFGPGPVLNKNNEVR
tr|Q7B8V4|Q7B8V4_CLOBO             GS-----TIDTELKVIDTNCINVIQPDGSYRSEEL-NLVIIGPSADIIQFECK
.*          .***: : : * ::      ...: * * **:*:*.. : : * :
```

```
unk|VIRT3669|Blast_submission      NKNYFPCRDGFGSIMQMAFCPEYVPTFDNVNIENITSLTIGKSKYFQDPALLLM
tr|Q7B8V4|Q7B8V4_CLOBO             NLT----RNGYGSTQYIRFSPDFTFGFEESLEVDTNPLLGAGKFATDPAVTLA
*          *:***:          : * * * :          *::: * *          : * : * :          ****: *
```

```
unk|VIRT3669|Blast_submission HGLYGMQVSSHEIIPSKQEIYMQHT-YPISAEELFTFGGQDANLISIDIKNDL
tr|Q7B8V4|Q7B8V4_CLOBO HRLYGIAINPNRVFKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDSLQENEF
* ***: : : : : : : * : : : * *** *****: : : : : : : : *
```

```
unk|VIRT3669|Blast_submission      YKAIANKLSQVTSCNDPNIDIDSYKQIYQQKYQFDKDSNGQYIVNEDKFQILY
tr|Q7B8V4|Q7B8V4_CLOBO             FKDIASLTlnKAksivGTTASLqYMKNVFKEkYLLSEdTSgKFSVDKLkFKDKLY
:* ** * : : * . . . : : * : : : : ** : : * : * : : * : : * : *
```

```
unk|VIRT3669|Blast_submission    TEIELGKKFNIKTRLSYFSMNHDPVKIPNLLDDTIYNDTEGFNIESKDLKSEY
tr|Q7B8V4|Q7B8V4_CLOBO          TEDNFVKFFKVLNRKTYLNFDAVKFI-NIVPKVNYTIYDGFNLNRTNLAANF
**  ::  *  *::  *  :*::::  .***:::  .  *  :****:..*  :::
```

```
unk|VIRT3669|Blast_submission NTNAF---RNVDGSLVSKLIGLCCKKIIPPTNIRENLYNRTASLTDLGGELCI
tr|Q7B8V4|Q7B8V4_CLOBO` NNMNF*TKLNFTGLFEFYKLLCVRGIITSKT:KS:L:DKGYNKALN-----DLCI
*      *      :*      *      ***:   :      *      *:      ::      **:      .      :****
```

```
unk|VIRT3669|Blast_submission      TFIAEKNSFSEEPFQDEIVSYNTKNKPLNFNYSLDKIIVDY-----NLQSKI
tr|Q7B8V4|Q7B8V4_CLOBO             FFSPSEDNFTNDLNKGEEITSDTNIEAAEENISLDLIQQYYLTFNFDNEPENI
*  . . . . * . . . .  . * . . . * . . . . * * * * *  *      *  . . *
```

```
unk|VIRT3669|Blast_submission      TPVTKGIPYAPEYKSNAASTIEIHNIDDNTIYQYLYAQKSPTTLQRITMTNSV
tr|Q7B8V4|Q7B8V4_CLOBO             SDIIGQLELMPNIERFPNG--KKYELDKYTMFHYLRAQEFEHGKSRIALTNSV
                                     :  :      *  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
                                     :  :      *  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
```

```
unk|VIRT3669|Blast_submission      TKIYSYFPS-VISKVNQGAQGILFLQWVRDIIDDFTNESQKTTIDKISDVST
tr|Q7B8V4|Q7B8V4_CLOBO             SRVYTFSSDYVKKVNKATEAAMFLGWVEQLVYDFTDETSEVSTTDKIADITI
                                     :.:*.:*.*.:****.:.:** **.:.:*****.:.:* ****.:.
```

```
unk|VIRT3669|Blast_submission    ALNIVKQGYEGNFIGALETGGVLLLEYIPEITLPVIAALSIAESSTQKEKII
tr|Q7B8V4|Q7B8V4_CLOBO          ALNIGNMLYKDDFVGALIFSGAVILLEFIPEIAIPVLGTFALVSYIANKVLTV
****      :  *::*:***  :*:*:*****:***:.....  :*:  :
```

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unk|VIRT3669|Blast_submission      EKRYEKWIEVYKLVKAKWLGTVNTQFQKRSYQMYRSLEYQVDAIKKIIDYEYK
tr|Q7B8V4|Q7B8V4_CLOBO             SKRNEKWDEVYKYIVTNWLAKVNTQIDLIRKKMKEALENQAEATKAIINQYN
                                     .** *** ***** : ::*:*****: :*:*** *: * *****:
```

```
unk|VIRT3669|Blast_submission      EQIADEINNLLKNKLEEKANKAMININIFMRESSRSFLVNQMQINEAKQLLEFD
tr|Q7B8V4|Q7B8V4_CLOBO             NNINFNIDDLSSKLNESINKAMININKFLNQCSVSYLMNSMIPYGVKRLDEFD
.:*  .*:.*  ***.*  *****  *.:.*  *.:*****  .  ***.  .**
```

```
unk|VIRT3669|Blast_submission MQYIKANSKFIGITELKKLESKINKVFSTPIPFSSYSKNLDCWVDNEEDIDVIL
tr|Q7B8V4|Q7B8V4 CLOBO LKYYIDNRGTL-IGQVDRCLKDKVNNTLSTDIPFQLSK----YVDNQRLSTFT
```

sp P10845 Botulinum neurotoxin type A precursor (EC 3.4.24.69)
 BXA1_CLOBO (BoNT/A)
 (Bontoxilysin-A) (BOTOX) [Contains: Botulinum
 neurotoxin
 A light-chain; Botulinum neurotoxin A heavy-chain]
 [botA]
 [Clostridium botulinum]

Score = 645 bits (1665), Expect = 0.0

Identities = 438/1339 (32%), Positives = 683/1339 (51%), Gaps = 77

Query: 1 PITINNFRYSDPVNNDTIIMMEPPYCKGLDIYYKAFKITDRIWIVPERYEFGTKP
 P F Y DPVN I ++ P + KAFKI ++IW++PER F T P
 Sbjct: 1 PFVNKQFNYKDPVNGVDIAYIKIPNVGQMOPV-KAFKIHNKIWVIPERDTF-TNP

Query: 59 NPPSSLIEGASEYYDPNYLRTDSDKDRFLQTMVKLFNRIKNNVAGEALLDKIINA
 NPP + YYD YL TD++KD +L+ + KLF RI + G LL I+
 Sbjct: 59 NPPPEAKQVPVSYDSTYLSTDNEKDNLYLKGVTCLFERIYSTDLGRMLLTSIVRG

Query: 119 NSY--SLLDKFDTNSNSVSFNLEQDPGATTKSAMLTNLIIFGPGPVLNKNEVR
 S + L DTN N+++ D S + + NL+I GP. + + E +
 Sbjct: 119 GSTIDTELKVIDTNC----INVIQPDGSYRSEE----LNLVIIGPSADIIQFECK

Query: 177 VDNKNYFPCRDGFGSIMQMAFCPEYVPTFDNVNIENITSLTIGKSKYFQDPALLM
 V N R+G+GS + F P++ F+ +E T+ +G K+ DPA+ L
 Sbjct: 171 VLNLTL----RNGYGSTQYIRFSPDFTFGFEESLEVDTNPLLGAAGKFDATDPAVTLA

Query: 237 VLHGLYGMQVSSHEIIPSKQEIIYMQHT-YPISAEELFTFGGQDANLISIDIKNDL
 H LYG+ ++ + + Y + + +S EEL TFGG DA I +N+
 Sbjct: 227 AGHRLYGIAINPNRVFKVNTNAYYEMSGLEVSFEELRTFGGHDAGFIDSLQENEF

Query: 296 NDYKAIANKLSQVTSCNDPNIDIDSYKQIYQQKYQFDKDSNGQYIVNEDKFQILY
 N +K IA+ L++ S + K ++++KY +D++G++ V++ KF LY
 Sbjct: 287 NKFKDIASTLNKAKSIVGTTASLQYMKNVFKEKYLLSEDTSGKFSVDKLFKFDKLY

Query: 356 GFTEIELGKKFNIKTRLSYFSMNHDPVKIPNLLDDTIYNDTEGFNIESKDLKSEY
 +TE K F + R +Y + + KI N++ Y +GFN+ + +L + +
 Sbjct: 347 IYTEDNFVKFFKVLNRKTYLNFDAVFKI-NIVPKVNYTIYDGFNLRNTNLAANF

Query: 416 RVNTNAF---RNVDGSGLVSKLIGLCKKIIPPTNIRENLYNRTASLTDLGELCI
 +N F +N G KL+ + I T + YN+ + +LCI
 Sbjct: 406 EINNMNFTKLKNFTGLFEFYKLLCVRGIITSKTKSLDKGYNKALN-----DLCI

Query: 473 DLTFIAEKNSFSEEPFQDEIVSYNTKNKPLNFNYSLDKIIVDY-----NLQSKI
 DL F +++F+ + + E ++ +T + N SLD I Y N I
 Sbjct: 460 DLFFSPSEDNFTNDLNKGEEITSDTNIEAAEENISLDLIQQYYLTNFNFDNEPENI

Query: 527 RTTPVTKGIPYAPEYKSNAASTIEIHNIDDNTIYQYLYAQKSPTTLQRITMTNSV


```

      ++ + + P + + + +D T++ YL AQ+ RI +TNSV
Sbjct: 519 LSSDIIGQLELMPNIERFPNG--KKYELDKYTMFHYLRAQEFEGHKSRIALTNSV

Query: 587 NSTKIYSYFPS-VISKVNQGAQGILFLQWVRDIIDDFTNESSQKTTIDKISDVST
      N +++Y++F S + KVN+ + +FL WV ++ DFT+E+S+ +T DKI+D++
Sbjct: 577 NPSRVYTFSSDYVKVKNKATEAAMFLGWVEQLVYDFTDETSEVSTTDKIADITI

Query: 646 GPALNIVKQGYEGNFIGALETGTGVVLLLEYIPEITLPVIAALSIAESSTQKEKII
      GPALNI Y+ +F+GAL +G V+LLE+IPEI +PV+ ++ K +
Sbjct: 637 GPALNIGNMLYKDDFVGALIFSGAVILLEFIPEIAIPVLGTFALVSYIANKVLTV

Query: 706 FLEKRYEKWIEVYKLVKAKWLGTVNTQFQKRSYQMYRSLEYQVDAXXXXXXXXXXX
      L KR EKW EVYK + WL VNTQ +M +LE Q +A
Sbjct: 697 ALSKRNEKWDEVYKYIVTNWLAKVNTQIDLIRKKMKEALENQAATKAIINYQYN

Query: 766 DKEQIADEIXXXXXXXXXXXXXXXXXMININIFMRESSRSFLVNQMINEAKKQLEFD
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Query: 826 ILMQYIKANSKFIGITELKKLESKINKVFSTPIPFSSYKLNDCWVDNEEDIDVIL
      L++YI N + I ++ +L+ K+N ST IPF SK +VDN+ +
Sbjct: 817 ALLKYIIDNRGTL-IGQVDRCLKDKVNNTLSTDIPFQLSK----YVDNQRLSTFT

Query: 883 --STXXXXXXXXXXXXXXXXXGFNSSVITYPDAQLVPGINGKAIHLVNNESESEVIVH
      +T +S I I+ I L N ESS++ V
Sbjct: 872 IINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVI

Query: 941 EYNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISSMKKHSLSIGSGWSVSLK
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Sbjct: 932 VYNSMYENFSTSFWIRIPKYFNSISL---NNEYTIINCMENN-----SGWKVSLN

Query: 1001 WTLKDSAGEVRQITFRDLDPKFNAYLANKWVFITITNDRLSSANLYINGVLMGSA
      WTL+D+ +++ F+ + N+W+F+TITN+RL+++ +YING L+
Sbjct: 984 WTLQDTQEIKQRVVFYKYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQK

Query: 1061 GAIREDDNNITLKLDRCNNNNQYVSIDKFRIECKALNPKEIEKLYTSYLSITFLRD
      G I NNI KLD C + ++Y+ I F +F K LN KEI+ LY + + L+D
Sbjct: 1044 GNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNNGILKD

Query: 1121 LRYDTEYYLIPVASSSKDVQLKN--ITDYMILTNAPSYTNGLNIIYYR-RLYNGL
      L+YD YY++ + +K V + N I YMYL P + NIY LY G
Sbjct: 1104 LQYDKPYMLNLYDPNKYVDVNNVGIRGYMYL-KGPRGSVMTTNIYLNSSLYRGT

Query: 1178 RYTPNNEIDSFVKSGDFIKLYVSYNNNEHIVGYPKDGNAFN-NLDRILRVGYNAP
      +Y N+ D+ V++ D + + V N E Y NA +++IL P
Sbjct: 1163 KYASGNK-DNIVRNNDRVYINVVVKNKE----YRLATNASQAGVEKILS-ALEIP

```

Query: 1237 KKMEAVKLRLDK--TYSVQLKLYDDKNASLGLVGTHNGQIGNDPNRDILIASNWY
++ +K ++ + T ++ L D+ +G +G H Q N L+ASNWY
Sbjct: 1217 SQVVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFH--QFNNIAK---LVASNWY

Query: 1295 --DKILGCDWYFVPTDEGW 1311
+ LGC W F+P D+GW
Sbjct: 1272 RSSRTLGCSEFIPVDDGW 1290

```

::** * : * ::*:**:*::** ** :***: . :. :
unk|VIRT3669|Blast_submission KSTILNLDINNDIISDISGFNSSVITYPDQLVPGINGKAIHLVNNESSEVIV
tr|Q7B8V4|Q7B8V4_CLOBO NTSILNLRYESNHLIDLSRYASKINIGSKVNFDP-IDKNQIQLFNLESSKIEV
::**** :. : *:* : *.: :. :. : * * : : *:* * ****: *
unk|VIRT3669|Blast_submission YNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISSMKKHLSLSIGSGWSVSL
tr|Q7B8V4|Q7B8V4_CLOBO YNSMYENFSTSFWIRIPKYFNSISL---NNEYTIINCMENN-----SGWKVSL
**.*:***:***:*:* * .***.*.*.*: : ***.***
unk|VIRT3669|Blast_submission TLKDSAGEVRQITFRDLPDKFNAYLANKWVFITITNDRLLSSANLYINGVLMGS
tr|Q7B8V4|Q7B8V4_CLOBO TLQDTQEIKQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQ
**.*: :. :.*: : *:*:*:****:*.*.:*** *:.
unk|VIRT3669|Blast_submission AIREDNNITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLSITFLR
tr|Q7B8V4|Q7B8V4_CLOBO NIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNNGILK
*: .*** :*** *.:***: * . *.* * * * ****:.* . . :*:
unk|VIRT3669|Blast_submission RYDTEYYLIPVASSSKDVQLKN--ITDYMILTNPASYTNGKLNIIYRR-LYNG
tr|Q7B8V4|Q7B8V4_CLOBO QYDKPYMLNLYDPNKYVDVNNVGIRGYMYL-KGPRGSVMTTNIYLNSSLYRG
:*. **:: : ...* *:::* * .***** :.* : . *** . **.*
unk|VIRT3669|Blast_submission YTPNNEIDSFVKSGDFIKLYVSYNNNEHIVGYPKDGNAFNNDLDRILRVGYNAP
tr|Q7B8V4|Q7B8V4_CLOBO YASGNK-DNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEI----P
*:.*: *:*:.* * : : * :*:*: :. . :. :. : *.: *
unk|VIRT3669|Blast_submission MEAVKLRLDK--TYSVQLKLYDDKNASLGLVGTHNGQIGNDPNRDILIASNWX
tr|Q7B8V4|Q7B8V4_CLOBO VVVMKSKNDQGITNKCKMNLQDNNNGNDIGFIGFHQF-----NNIAKLVASNW
: .:* :. : * . :.* *:. .*:*: * * : * . :. :
unk|VIRT3669|Blast_submission KDKILGCDWYFVPTDEGWTND--
tr|Q7B8V4|Q7B8V4_CLOBO SSRTLGCSEFIPVDDGWERPL
... ***.* *:*.*:* * :

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CLUSTAL FORMAT for T-COFFEE Version_1.37, CPU=0.00 sec, SCORE=3830, Nseq=2, Len=1337

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unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      PFVVKQFNYKDPVNGVDIAYIKIPNVGQMOPVKAFKIHNKIWVIPERDTFTNP

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      PPEAKQVPVSYDSTYLSTDNEKDNLYLKGVTKLFERIYSTDLGRMLLTSIVRG

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      TIDTELKVIDTNCINVIQPDGSYRSEELNLVIIGPSADIIQFECKSFGHEVLN

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      STQYIRFSPDFTFGFEESLEVDTNPLLGAAGKFATDPAVTLAHELIHAGHRLYG

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      VFKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYYNKFKDIA

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      -LYNRTASLTDLGG-----
SIVGTTASLQYMKNVFKEYLLSEDTSGKFSVDKLKFDKLYKMLTEIYTEDNF
: . **** : .

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      NRKTYLNFDKAVFKINIVPKVNYTIYDGFNLRNTNLAANFNGQNTNINNMNFT

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      -----ELCIKIKNEDLTFIAEKNSFSEE
LFEFYKLLCVRGIITSKTKSLDKGYNKALNDLCIKVNNWDLFFSPSEDNFTND
:****::* ** * .....*:::

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      SYNTKNKPLNFNYSLDKIIVDY-----NLQSKITLPNDRTTPV--TKGIPYA
TSDTNIEAAEENISLDLIQQYYLTFNFDNEPENISNIENLSSDIIGQLELMPNI
:.*:.. : * *** * * * ..::: * : : :.*

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      ASTIEIHNIDDNTIYQYLYAQKSPTTLQRITMTNSVDDALINSTKIYSYFSPV
KYELDKYTMFHYLRAQEFEGKSRIALTNSVNEALLNPSRVYTFSSDY----
: : : . * : ** :* . . : : : : .*

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      AQGILFLQWVRDIIDDFTNESSQKTTIDKISDVSTIVPYIGPALNIVKQGYEG
TEAAMFLGWVEQLVYDFTDETSEVSTTDKIADITIIIPYIGPALNIGNMLYKD
:.. :.* ** ..::: ***:*:* :* ***:*:* :***** :*:.

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      TTGVVLLLEYIPEITLPVIAALSIAESSTQKEKIIKTIDNFLEKRYEKWIEVY
FSGAVILLEFIPEIAIPVLGTFALVSYIANKVLTQVQIDNALSKEKWDDEVY
:*.*:***:*****:*:..... :.* :***** *.* ** **

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      LGTVNTQFQKRSYQMYRSLEYQVDAIKKIIDYEYKIYSGPDKEQIADENNLK
LAKVNTQIDLIRKKMKEALENQAATKAIINYQYNQYTEEEKNNINFNIDDL
*..*****: :* :.* ** *.* * **:*:* :* :*:.* :*:.*

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      NKAMININIFMRESSRSFLVNQMINAEAKKQLLEFDTQSKNILMQYIKANSKFI
NKAMININKFLNQCSVSYLMNSMIPYGVKRLEDFDASLKDALLKYIYDNRG--
***** *:::* *:*:*.* . *:* :*:.. * :*:** *

unk|VIRT5247|Blast_submission -----
sp|P10845|BXA1_CLOBO      LESKINKVFSTPIPFYSYKNLDCWVDNEEDIDVILKKSTILNLDINNDIISDI
VDRLKDKVNNT-----LSTDIPFQLSKYVDNQRLSTFTEYIKNIINTSILNL

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::      : ** . *      * . : :      : : * : : * . . *      : * * * * : :

unk|VIRT5247|Blast_submission  ITYPDAQLVPGINGKA-----IHLVNNESESVIVHKAMDIEYNDMFNNF
sp|P10845|BXA1_CLOBO          IDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENF
* . . . . . * . . . . . * : * . * * * : : * * * * . : : * *

unk|VIRT5247|Blast_submission  VPKVSASHLEQYGTNEYSIISSMKKHSLSIGSGWSVSLKGNLIWTLKDSAGE
sp|P10845|BXA1_CLOBO          IPKYFNSISL---NNEYTIINCMENN-----SGWKVSLNYGEIIWTLQDTQEI
: * * * * . * * * . * * : : : * * * * * : : : * * * * : :

unk|VIRT5247|Blast_submission  DLPDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIRDNNI
sp|P10845|BXA1_CLOBO          YSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI
: * : * : * * * : * * . : : : * * * * * : : * : * * * : * *

unk|VIRT5247|Blast_submission  NNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLSITFLRDFWGNPLRYDTEYYL
sp|P10845|BXA1_CLOBO          RDTHRYIWIKYFNLFDKELNEKEIKDLYDNQNSGILKDFWGDYLYDKPYYM
. : : : * : * . * : * * * * * : * * . . : * : * * * : * : * * :

unk|VIRT5247|Blast_submission  KDVQLKNITDYMVL-----TNAPSYTNGKLNIIYRRLYNGLKFIKRYTPNNE
sp|P10845|BXA1_CLOBO          KYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI
* * : : * : * : * : * * * * * : : * : * : * : * : *

unk|VIRT5247|Blast_submission  VKSGDFIKLYVSYNNNEHIVGYPKDGNAFNNLDRILRVGYNAPGIPLYKKMEA
sp|P10845|BXA1_CLOBO          YINVVVKNKEYRLATNASQAGVEKILSALEIPD----VGNLSQVVVMKSKND-
. . : . * . * * . * : : * * * : : : * :

unk|VIRT5247|Blast_submission  TYSVQLKLYDDKNASLGLVGTHNGQ-----IGNDPNRDI-----LIASNWYF
sp|P10845|BXA1_CLOBO          TNKCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWYNRQIERSSRTLGCSEF
* . : : * * : . : : * * : : * * * * : : * * * : : * *

unk|VIRT5247|Blast_submission  LGCDWYFVPTDEGWTND
sp|P10845|BXA1_CLOBO          ---GWERPL-----
. * *

```

☐ 1: Autoimmunity. 1998;27(2):79-90.

[Links](#)

T cell responses in EAMG-susceptible and non-susceptible mouse strains after immunization with overlapping peptides encompassing the extracellular part of Torpedo californica acetylcholine receptor alpha chain. Implication to role in myasthenia gravis of autoimmune T-cell responses against receptor degradation products.

Oshima M, Yokoi T, Deitiker P, Atassi MZ.

Verna and Marrs McLean Department of Biochemistry, Baylor College of Medicine, Houston, TX 77030, USA.

To study the role in myasthenia gravis (MG) of peptides resulting from acetylcholine receptor (AChR) degradation, we examined the ability of AChR peptides to induce T cell responses that are capable of cross-reacting with intact AChR. The studies were carried out in an experimental autoimmune MG (EAMG)-susceptible mouse strain [C57BL/6 (B6)] as well as in two non-susceptible strains [B6.C-H-2bm12 (bm12) and C3H/He]. A set of overlapping peptides encompassing the extracellular part (residues 1-210) of the alpha-chain of Torpedo californica (t) AChR were used, individually or in equimolar mixtures, as immunogens. In B6, immunization with peptides alpha45-60, alpha111-126, alpha146-162 and alpha182-198 gave T cells that responded in vitro to the correlate immunizing peptide. Only the T cells against the latter three peptides cross-reacted with tAChR. Peptide alpha146-162 exhibited the highest in vitro reaction with the immunizing peptide and cross-reaction with tAChR. T cells obtained by immunization of B6 with an equimolar mixture of the peptides responded in vitro to peptides alpha111-126, alpha146-162 and alpha182-198 and cross-reacted very strongly with tAChR. In bm12 and C3H/He, a number of peptides evoked, when used individually as immunogens, strong or moderate T cell responses that recognized in vitro the correlate immunizing peptide but cross-reacted poorly with tAChR. Immunization with the mixture of the peptides gave T cells that recognized several peptides in each strain but did not cross-react with alpha146-162 or tAChR. The results indicate that the ability to recognize alpha146-162 or AChR by T cells against peptides resulting from receptor degradation can account for the susceptibility to, and aggravation of, MG in B6.

PMID: 9583739 [PubMed - indexed for MEDLINE]



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☐ 1: [Eur J Epidemiol. 1992 Jan;8\(1\):1-8.](#)

[Links](#)

Characteristics of toxin-neutralization by anti-tetanus human monoclonal antibodies directed against the three functional domains [A], [B] and [C] of the tetanus toxin molecule and a reliable method for evaluating the protective effects of monoclonal antibodies.

Matsuda M, Kamei M, Sugimoto N, Ma Y, Hashizume S.

Department of Tuberculosis Research, Osaka University, Japan.

Five anti-tetanus human monoclonal antibodies (MAbs) produced by hybrid cell lines we established previously were characterized. Their abilities to neutralize tetanus toxin in vitro and to protect mice against challenge with toxin were studied by observing the changes in the progress of symptoms in mice. Immunostaining showed that MAbs MAb-G4 and G2 recognized the N-terminal domain, [A] and the C-terminal domain, [C] of the tetanus toxin molecule, respectively, while MAbs MAb-G1, G3 and G6 recognized its middle domain, [B]. Enzyme-linked immunosorbent assay showed that the binding affinity of MAb-G3 was 2.9×10^{10} M⁻¹ and those of the other MAbs were as high as approximately 10^{11} M⁻¹. In in vitro neutralization experiments, at sufficient doses all the MAbs as single reagents protected mice completely against the effect of tetanus toxin. However, at lower doses than those sufficient to rescue mice, the kinetic patterns of progress of symptoms with the individual MAbs differed with each other and, except for MAb-G4, were different from that of anti-tetanus human polyclonal antibody. They suppressed the development and/or slowed the rate of progress of symptoms for over 96 h and delayed death of the mice. We propose that the comparison of the minimum survival dose with that of human polyclonal antibody of known international units is a reliable method for estimating the actual protective activity of a MAb. Intravenous (IV) injection of doses of individual MAbs or their mixtures at over 0.03 IU per mouse protected mice from subsequent challenge with 20 MLD of tetanus toxin. (ABSTRACT TRUNCATED AT 250 WORDS)

PMID: 1572415 [PubMed - indexed for MEDLINE]

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Characteristics of toxin-neutralization by anti-tetanus human monoclonal antibodies directed against the three functional domains [A], [B] and [C] of the tetanus toxin molecule and a reliable method for evaluating the protective effects of monoclonal antibodies.

Matsuda M, Kamei M, Sugimoto N, Ma Y, Hashizume S.

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PMID: 1572415 [PubMed - indexed for MEDLINE]

☐ 1: Hybridoma. 1986 Spring;5(1):21-31.

[Links](#)

Protection of mice against tetanus toxin by combination of two human monoclonal antibodies recognizing distinct epitopes on the toxin molecule.

Ziegler-Heitbrock HW, Reiter C, Trenkmann J, Futterer A, Riethmuller G.

Human B-lymphocytes were fused with the human lymphoblastoid B-cell line WI-L2-729 HF2. Hybridoma frequencies were in the range of 10^{-5} when the mononuclear cells were (a) prestimulated with pokeweed mitogen (PWM), (b) fused with polyethyleneglycol (PEG), and (c) selected in a hypoxanthine-azaserine (HAza) containing medium. To generate monoclonal antibodies (MAb) specific for tetanus toxin (TToxin) human spleen cells were precultured with PWM plus tetanus toxoid (TToxoid) in two separate fusions. Two hybridomas were selected based on high binding activity using an enzyme-linked immunosorbent assay (ELISA) for TToxoid. Both hybridomas, cloned twice and designated anti-TT1 and anti-TT2, exhibited a near tetraploid karyotype and showed stable production of antibody (0.15 micrograms/ml) over several months. Using ELISA for fragments of TToxin and the immunoblotting technique, the two IgG1 monoclonal antibodies were found to bind to the heavy chain portion of the B-fragment (anti-TT1) and on the C-fragment (anti-TT2) of the toxin. When tested in an ELISA with TToxin the combination of anti-TT1 and anti-TT2 showed higher binding activity than either reagent alone. In an in vivo neutralization assay mice were completely protected against TToxin by the combination of the two antibodies while either antibody alone resulted only in a delay of death of the mice. These findings demonstrate that a cocktail of appropriate human monoclonal antibodies can be far superior to a single reagent when used in a therapeutic setting.

PMID: 2420699 [PubMed - indexed for MEDLINE]

☐ 1: Mol Immunol. 1994 Oct;31(15):1141-8.

[Links](#)

Synthetic peptide antigens of tetanus toxin.

Fischer PM, Howden ME.

Department of Biological Sciences, Deakin University, Geelong, Victoria, Australia.

In this study the immunochemical structure of the heavy chain polypeptide from tetanus toxin was studied. Numerous antigenic determinants were identified by probing a set of overlapping peptides derived from the amino acid sequence of tetanus toxin with polyclonal anti-toxoid antibody preparations. Synthetic antigens representing continuous epitopes were prepared and used to immunize mice. The capacity of the resulting anti-peptide antibodies to react with tetanus toxin in vitro and in vivo was determined. The majority of antibodies bound to tetanus toxin and three epitopes capable of eliciting neutralizing antibodies were identified.

Mavoungou E, Toure FS, Yaba P, Delicat A, Poaty-Mavoungou V.

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Peptide immunization restimulates the memory CD4 T cell response but fails to induce cytotoxic T lymphocytes in cynomolgus monkeys.

J Med Primatol. 1998 Aug;27(4):202-9.

PMID: 9879861 [PubMed - indexed for MEDLINE]

☐ 1: Chin Med J (Engl). 1999 Aug;112(8):691-7.

[Links](#)

A recombinant multi-epitope, multi-stage malaria vaccine candidate expressed in *Escherichia coli*.

Li M, Bi H, Dong W, Xu W, Li Q, Li Y.

Institute of Tropical Medicine, First Military Medical University, Guangzhou, 510515, China.

OBJECTIVE: To construct and evaluate a recombinant multi-epitope, multistage malaria vaccine candidate expressed in *Escherichia coli* (*E. coli*). **METHODS:** A hybrid gene (HGF) encoding several putative immunodominant T or T/B epitopes from MSP-1, MSP-2, Pf155/RESA of *Plasmodium falciparum* (*P. falciparum*) and two immune-stimulating epitopes from interleukin-1 and tetanus toxin was synthesized. Two copies of HGF and a copy of gene encoding Pattaroyo's Spf66 were connected together to construct a sandwich hybrid gene HGFSP. The gene was cloned into an expression vector pWR450-I for production of a fusion protein with beta-galactosidase. Efficacy of this vaccine candidate in inducing specific immunity against malaria parasites was evaluated. **RESULTS:** Immunization of different species of animals with purified recombinant peptide showed that the peptide was able to induce remarkable antibody response to the immunized peptide as well as *falciparum* malaria parasites. The epitopes included in the construct could induce antibodies against the intact parasite proteins as demonstrated by western blotting, indicating the epitopes retained their antigenicity in the new peptide construct. Antibodies from animals immunized with recombinant HGFSP peptide exhibited good ability in inhibition of the *in vitro* growth of malaria parasites, augmentation of phagocytosis of the parasites or infected RBC by phagocytes, and facilitation of antibody dependent cell mediated cytotoxicity to the cultured malaria parasites. **CONCLUSION:** The recombinant peptide seems to be a potential candidate which is valuable for further investigation.

PMID: 11601273 [PubMed - indexed for MEDLINE]

: Mol Immunol. 1994 Oct;31(15):1141-8.

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Synthetic peptide antigens of tetanus toxin.

Fischer PM, Howden ME.

Department of Biological Sciences, Deakin University, Geelong,
Victoria, Australia.

In this study the immunochemical structure of the heavy chain polypeptide from tetanus toxin was studied. Numerous antigenic determinants were identified by probing a set of overlapping peptides derived from the amino acid sequence of tetanus toxin with polyclonal anti-toxoid antibody preparations. Synthetic antigens representing continuous epitopes were prepared and used to immunize mice. The capacity of the resulting anti-peptide antibodies to react with tetanus toxin in vitro and in vivo was determined. The majority of antibodies bound to tetanus toxin and three epitopes capable of eliciting neutralizing antibodies were identified.

PMID: 7935502 [PubMed - indexed for MEDLINE]

J Infect Dis. 1997 Feb;175(2):382-91.

[Links](#)

Epitope repertoire of human CD4+ T cells on tetanus toxin: identification of immunodominant sequence segments.

Diethelm-Okita BM, Raju R, Okita DK, Conti-Fine BM.

Department of Biochemistry, College of Biological Sciences, University of Minnesota, St. Paul 55108, USA.

Sequence regions of tetanus toxin-forming CD4+ cell epitopes in 8 HLA-disparate subjects were identified. Overlapping synthetic peptides corresponding to the complete tetanus toxin sequence were used to test, in a proliferation assay, unselected blood CD4+ cells or CD4+ cell lines propagated by stimulation with tetanus toxoid. The CD4+ cell lines recognized most peptides recognized by the blood CD4+ cells and they recognized additional peptides. Their responses were stronger than those of unselected blood CD4+ cells. Two peptides were recognized by all subjects: one largely overlapped a tetanus toxin sequence region previously identified as a "universal" T cell epitope. Thirteen other peptides elicited a CD4+ cell response in 6 or 7 of the 8 subjects, and another 10 elicited responses in 5 subjects.

PMID: 9203659 [PubMed - indexed for MEDLINE]

CLUSTAL W (1.82) multiple sequence alignment

sp P04958 TETX_CLOTE	-PITINNFRYSDPVNNDTIIMMEPPYCKGLDIYYKAFKITDRIWIVPERD
tr Q7B8V4 Q7B8V4_CLOBO	MPFVNKQFNYKDPVNGVDIAYIKIPNAG-QMQPVKAFKIHNKIWIWIPERD
sp P10845 BXA1_CLOBO	-PFVNKQFNYKDPVNGVDIAYIKIPNVG-QMQPVKAFKIHNKIWIWIPERD
tr Q2PPK6 Q2PPK6_CLOBO	MPFVNKQFNYKDPVNGVDIAYIKIPNAG-QMQPVKAFKIHNKIWIWIPERD
sp Q45894 BXA2_CLOBO	-PFVNKQFNYKDPVNGVDIAYIKIPNAG-QMQPVKAFKIHNKIWIWIPERD
tr Q3LRX8 Q3LRX8_CLOBO	MPLVNQQINYYDPVNGVDIAYIKIPNAG-KMQPVKAFKIHNKVWVWIPERD
	.: :.:. *****. * :. * ***** :.:.:***
sp P04958 TETX_CLOTE	EFGTKPE-DFNPPSSLIEGASEYYDPNYLRTSDSKDRFLQTMVKLFNRK
tr Q7B8V4 Q7B8V4_CLOBO	TFTNPEEGDLNPPPEAKQVPVSYDDSTYLSTDNEKDNYLKGVTKLFERIY
sp P10845 BXA1_CLOBO	TFTNPEEGDLNPPPEAKQVPVSYDDSTYLSTDNEKDNYLKGVTKLFERIY
tr Q2PPK6 Q2PPK6_CLOBO	TFTNPEEGDLNPPPEAKQVPVSYDDSTYLSTDNEKDNYLKGVTKLFERIY
sp Q45894 BXA2_CLOBO	TFTNPEEGDLNPPPEAKQVPVSYDDSTYLSTDNEKDNYLKGVTKLFERIY
tr Q3LRX8 Q3LRX8_CLOBO	IFTNPEEVDLNPPPEAKQVPISYYDSAYLSTDNEKDNYLKGVTKLFERIY
	* . * *:***.. : . ***** ** **.:**.:* : ***:**
sp P04958 TETX_CLOTE	NNVAGEALLDKIINAIPLYGNSYSLDDKFDTSNSVSFNLLQDPDGATT
tr Q7B8V4 Q7B8V4_CLOBO	STDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDG-----S
sp P10845 BXA1_CLOBO	STDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDG-----S
tr Q2PPK6 Q2PPK6_CLOBO	STDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDG-----S
sp Q45894 BXA2_CLOBO	STDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDG-----S
tr Q3LRX8 Q3LRX8_CLOBO	STDLGRMLLTSIVRGIPFWGGGKIDTELKVIDTNCINIIQLDD-----S
	.. *. ** *.:***: *.. : :*:*** : :
sp P04958 TETX_CLOTE	KSAMLTNLIIFGPGPVLNKNNEVRGIVLRVDNKNYFPCRDGFGSIMQMAFC
tr Q7B8V4 Q7B8V4_CLOBO	YRSEELNLVIIIGPSADIIQFECKSFGHEVLN----LTRNGYGSTQYIRFS
sp P10845 BXA1_CLOBO	YRSEELNLVIIIGPSADIIQFECKSFGHEVLN----LTRNGYGSTQYIRFS
tr Q2PPK6 Q2PPK6_CLOBO	YRSEELNLVIIIGPSADIIQFECKSFGHDVLN----LTRNGYGSTQYIRFS
sp Q45894 BXA2_CLOBO	YRSEELNLVIIIGPSADIIQFECKSFGHDVLN----LTRNGYGSTQYIRFS
tr Q3LRX8 Q3LRX8_CLOBO	YRSEELNLAIIGPSANIIIESQCSSFRDDVLN----LTRNGYGSTQYIRFS
	: ** *:***. : : : .: * * *:*** : *
sp P04958 TETX_CLOTE	PEYVPTFDNVIENTISLTIGKSKYFQDPALLMHელიHVLHGLYGMQVSS
tr Q7B8V4 Q7B8V4_CLOBO	PDFTFGFEESELEVDTNPLLGAGKFATDPAVTLAელიHAGHRLYGIAINP
sp P10845 BXA1_CLOBO	PDFTFGFEESELEVDTNPLLGAGKFATDPAVTLAელიHAGHRLYGIAINP
tr Q2PPK6 Q2PPK6_CLOBO	PDFTFGFEESELEVDTNPLLGAGKFATDPAVTLAელიHAEHRLYGIAINP
sp Q45894 BXA2_CLOBO	PDFTFGFEESELEVDTNPLLGAGKFATDPAVTLAელიHAEHRLYGIAINP
tr Q3LRX8 Q3LRX8_CLOBO	PDFTVGFEESELEVDTNPLLGAGKFAQDPAVALAელიHAEHRLYGIAINT
	*.:. *: :.* . :.* :. ***: * *****. * ***: .:
sp P04958 TETX_CLOTE	HEIIPSKQEIYMQHT-YPISAEELFTFGGDANLISIDIKNDLYEKTLDN
tr Q7B8V4 Q7B8V4_CLOBO	NRVFKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYYNK
sp P10845 BXA1_CLOBO	NRVFKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYYNK
tr Q2PPK6 Q2PPK6_CLOBO	NRVFKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYYNK
sp Q45894 BXA2_CLOBO	NRVFKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYYNK
tr Q3LRX8 Q3LRX8_CLOBO	NRVFKVNTNAYYEMAGLEVSLEELITFGGNDAKFIDSLQKKEFSLYYYNK
	:.: : : * : : : * *** *****:***:*. :.: *
sp P04958 TETX_CLOTE	YKAIANKLSQVTSCNDPNIDIDSYKQIYQQKYQFDKDSNGQYIVNEDKFQ
tr Q7B8V4 Q7B8V4_CLOBO	FKDIASTLNKAKSIVGTASLQYMKNVFKEKYLLSEDTSKGFSVDKLKFD
sp P10845 BXA1_CLOBO	FKDIASTLNKAKSIVGTASLQYMKNVFKEKYLLSEDTSKGFSVDKLKFD
tr Q2PPK6 Q2PPK6_CLOBO	FKDVASTLNKAKSIIGTASLQYMKNVFKEKYLLSEDTSKGFSVDKLKFD
sp Q45894 BXA2_CLOBO	FKDVASTLNKAKSIIGTASLQYMKNVFKEKYLLSEDTSKGFSVDKLKFD
tr Q3LRX8 Q3LRX8_CLOBO	FKDIASTLNKAKSIVGTASLQYMKNVFKEKYLLSEDATGKFLVDRLKFD
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sp P04958 TETX_CLOTE	ILYNSIMYGFTEIELGKKFNIKTRLSYFSMNHDPVKIPNLLDDTIYNDTE

tr Q7B8V4 Q7B8V4_CLOBO	KLYKMLTEIYTEDNFVKFFKVLNRKTYLNFDKAVFKIN-IVPKVNYTIYD
sp P10845 BXA1_CLOBO	KLYKMLTEIYTEDNFVKFFKVLNRKTYLNFDKAVFKIN-IVPKVNYTIYD
tr Q2PPK6 Q2PPK6_CLOBO	KLYKMLTEIYTEDNFVNFFKVINRKYLNFDKAVFRIN-IVPDENYTIKD
sp Q45894 BXA2_CLOBO	KLYKMLTEIYTEDNFVNFFKVINRKYLNFDKAVFRIN-IVPDENYTIKD
tr Q3LRX8 Q3LRX8_CLOBO	ELYKLLTEIYTEDNFVKFFKVLNRKTYLNFDKAVFKIN-IVPDVNYTIHD
	** : : : ** : : : * : : . * : * : : : . : * : : . * . :
sp P04958 TETX_CLOTE	GFNIESKDLKSEYKGQNMVRVNTNAFRNVD-GSGLVSKLIGLCKKIIPPTN
tr Q7B8V4 Q7B8V4_CLOBO	GFNLRTNLAANFNGQNTNINNMNFTKLKNFTGLFEFYKLLCVRGIITSK
sp P10845 BXA1_CLOBO	GFNLRTNLAANFNGQNTNINNMNFTKLKNFTGLFEFYKLLCVRGIITSK
tr Q2PPK6 Q2PPK6_CLOBO	GFNLKGANLSINFNGQNTNINSRNFTRLKNFTGLFEFYKLLCVRGIIPFK
sp Q45894 BXA2_CLOBO	GFNLKGANLSTNFNGQNTNINSRNFTRLKNFTGLFEFYKLLCVRGIIPFK
tr Q3LRX8 Q3LRX8_CLOBO	GFNLRTNLAANFNGQNTNINNMNFTKLKNFTGLFEFYKLLCVRGIITSK
	*** : . . : * : : : *** : . . : * : . . : * : : * : : :
sp P04958 TETX_CLOTE	IRENLYNRTASLTDLGGELCIKIKNEDLTFIAEKNSFSEEPFQDEIVSYN
tr Q7B8V4 Q7B8V4_CLOBO	TKSLDKGYNKALN----DLCIKVNNDLFFSPSEDNFTNDLNKGEEITS
sp P10845 BXA1_CLOBO	TKSLDKGYNKALN----DLCIKVNNDLFFSPSEDNFTNDLNKGEEITS
tr Q2PPK6 Q2PPK6_CLOBO	TKSLDEGYNKALN----DLCIKVNNDLFFSPSEDNFTNDLDKVEEITAD
sp Q45894 BXA2_CLOBO	TKSLDEGYNKALN----DLCIKVNNDLFFSPSEDNFTNDLDKVEEITAD
tr Q3LRX8 Q3LRX8_CLOBO	TKSLDEGYNKALN----ELCIKVNNDLFFSPSEDNFTNDLDKVEEITS
	: . . . : * . : : * : : : * * * * . . . : : * : : :
sp P04958 TETX_CLOTE	TKNKPLNFNYSLDKIIVDYNLQSKITLPNDRTP---VTKGIPYAPEYKS
tr Q7B8V4 Q7B8V4_CLOBO	TNIEAAEENISLDLIQQYYLTFNFDNEPENISIE NLSSDIIGQLELMPNI
sp P10845 BXA1_CLOBO	TNIEAAEENISLDLIQQYYLTFNFDNEPENISIE NLSSDIIGQLELMPNI
tr Q2PPK6 Q2PPK6_CLOBO	TNIEAAEENISLDLIQQYYLTFDFDNEPENISIE NLSSDIIGQLEPMPNI
sp Q45894 BXA2_CLOBO	TNIEAAEENISLDLIQQYYLTFDFDNEPENISIE NLSSDIIGQLEPMPNI
tr Q3LRX8 Q3LRX8_CLOBO	TNIEAAEENISLDLIQQYYLNFNFDNEPENTSIE NLSSDIIGQLEPMPNI
	* : . . : * * * * * . . . * : : : :
sp P04958 TETX_CLOTE	NAASTIEIHNIDDNTIYQYLYAQKSPTTLQORITMTNSVDDALINSTKIYS
tr Q7B8V4 Q7B8V4_CLOBO	ERFPNGKKYELDKYTMFHYLRAQEFEHGKSRIALTNSVNEALLNPSRVYT
sp P10845 BXA1_CLOBO	ERFPNGKKYELDKYTMFHYLRAQEFEHGKSRIALTNSVNEALLNPSRVYT
tr Q2PPK6 Q2PPK6_CLOBO	ERFPNGKKYELDKYTMFHYLRAQEFEHGDSRIILTNSAEEALLKPNVAYT
sp Q45894 BXA2_CLOBO	ERFPNGKKYELDKYTMFHYLRAQEFEHGDSRIILTNSAEEALLKPNVAYT
tr Q3LRX8 Q3LRX8_CLOBO	ERFPNGKKYELNKYTMFHYLRAQEFKHSNSRIILTNSAKEALLKPNIVYT
	: . . : : : : * : : * * : . . . * : : * : : * : : *
sp P04958 TETX_CLOTE	YFPS-VISKVNQGAQGILFLQWVRDIIDDFTNESSQKTTIDKISDVSTIV
tr Q7B8V4 Q7B8V4_CLOBO	FFSSDYVKKVNKATEAAMFLGWVEQLVYDFTDETSEVSTTDKIADITIII
sp P10845 BXA1_CLOBO	FFSSDYVKKVNKATEAAMFLGWVEQLVYDFTDETSEVSTTDKIADITIII
tr Q2PPK6 Q2PPK6_CLOBO	FFSSKYVKKINKAVEAFMFLNWAEELVYDFTDETNEVTTMDKIADITII
sp Q45894 BXA2_CLOBO	FFSSKYVKKINKAVEAFMFLNWAEELVYDFTDETNEVTTMDKIADITII
tr Q3LRX8 Q3LRX8_CLOBO	FFSSKYIKAINKAVEAVTFVNWIE NLVYDFTDETNEVSTMDKIADITIVI
	: * . * . . : * : : . . : * : * . . : * : * : * : : * : : *
sp P04958 TETX_CLOTE	PYIGPALNIVKQGYEGNFIGALETTGVVLLLEYIPEITLPVIAALSIAES
tr Q7B8V4 Q7B8V4_CLOBO	PYIGPALNIGNMLYKDDFVGALIFSGAVILLEFIPEIAIPVLGTFALVSY
sp P10845 BXA1_CLOBO	PYIGPALNIGNMLYKDDFVGALIFSGAVILLEFIPEIAIPVLGTFALVSY
tr Q2PPK6 Q2PPK6_CLOBO	PYIGPALNIGNMLSKGEFVEAIIFTGVVAMLEFIPEYALPVFGTFAIVSY
sp Q45894 BXA2_CLOBO	PYIGPALNIGNMLSKGEFVEAIIFTGVVAMLEFIPEYALPVFGTFAIVSY
tr Q3LRX8 Q3LRX8_CLOBO	PYIGPALNIGNMIYKGEFVEAIIFTSGAVILLEIVPEIALPVLGTFALVSY
	***** : . : : * : : * . * : * : * : * : * : * : *
sp P04958 TETX_CLOTE	STQKEKIIKTIDNFLEKRYEKWIEVYKLVKAKWLGTVNTQFQKRSYQMYR
tr Q7B8V4 Q7B8V4_CLOBO	IANKVLTVQTI DNALSKRNEKWDEVYKYIVTNWLAKVNTQIDLIRKKMKE
sp P10845 BXA1_CLOBO	IANKVLTVQTI DNALSKRNEKWDEVYKYIVTNWLAKVNTQIDLIRKKMKE
tr Q2PPK6 Q2PPK6_CLOBO	IANKVLTVQTI NNALSKRNEKWDEVYKYIVTNWLAKVNTQIDLIREKMKK
sp Q45894 BXA2_CLOBO	IANKVLTVQTI NNALSKRNEKWDEVYKYIVTNWLAKVNTQIDLIREKMKK

tr Q3LRX8 Q3LRX8_CLOBO	VSNKVLTVQOTIDNALSKRNEKWDEVYKYIVTNWLAIVNTQINLIREKMKK .: * :.: *.: *.: *.: *.: *.: *.: *.: *.: *.: *
sp P04958 TETX_CLOTE	SLEYQVDAIKKIIDYEEKIYSGPDKEQIADEINNKNKLEEKANKAMINI
tr Q7B8V4 Q7B8V4_CLOBO	ALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINKAMINI
sp P10845 BXA1_CLOBO	ALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINKAMINI
tr Q2PPK6 Q2PPK6_CLOBO	ALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINSAMINI
sp Q45894 BXA2_CLOBO	ALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINSAMINI
tr Q3LRX8 Q3LRX8_CLOBO	ALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINSAMINI : * * :.: *.: *.: *.: *.: *.: *.: *.: *.: *.: *
sp P04958 TETX_CLOTE	NIFMRESSRSFLVNQMINEAKKQLLEFDTQSKNILMQYIKANSKFIGITE
tr Q7B8V4 Q7B8V4_CLOBO	NKFLNQCSVSYLMNSMIPYGVKRLEDFDASLKDALLKYIYDN-RGTLIGQ
sp P10845 BXA1_CLOBO	NKFLNQCSVSYLMNSMIPYGVKRLEDFDASLKDALLKYIYDN-RGTLIGQ
tr Q2PPK6 Q2PPK6_CLOBO	NKFLDQCSVSYLMNSMIPYAVKRLKDFDASVRDVLKYYIYDN-RGTLVLQ
sp Q45894 BXA2_CLOBO	NKFLDQCSVSYLMNSMIPYAVKRLKDFDASVRDVLKYYIYDN-RGTLVLQ
tr Q3LRX8 Q3LRX8_CLOBO	NKFLDQCSVSYLMNSMIPYAVKRLKDFDASVRDVLKYYIYDN-RGTLIGQ * * :.: *.: *.: *.: *.: *.: *.: *.: *.: *.: *
sp P04958 TETX_CLOTE	LKKLESKINKVFSTPIPFYSYKNLD--CWVDNEEDIDVILKKSTILNLDI
tr Q7B8V4 Q7B8V4_CLOBO	VDRLKDKVNNTLSTDIPFQLSKYVDNQRLSTFTEYIKNIINTSILNLRY
sp P10845 BXA1_CLOBO	VDRLKDKVNNTLSTDIPFQLSKYVDNQRLSTFTEYIKNIINTSILNLRY
tr Q2PPK6 Q2PPK6_CLOBO	VDRLKDEVNNTLSADIPFQLSKYVDNKKLLSTFTEYIKNIVNTSILSIVY
sp Q45894 BXA2_CLOBO	VDRLKDEVNNTLSADIPFQLSKYVDNKKLLSTFTEYIKNIVNTSILSIVY
tr Q3LRX8 Q3LRX8_CLOBO	VNRLKDKVNNTLSADIPFQLSKYVDNKKLLSTFTEYIKNITNASILSIVY :.: *.: *.: *.: *.: *.: *.: *.: *.: *.: *
sp P04958 TETX_CLOTE	NNDIISDISGFNSSVITYPDAQLVPGINGKAIHLVNNESESEVIVHKAMDI
tr Q7B8V4 Q7B8V4_CLOBO	ESNHLIDLRLRYASKINIGSKVNFDP-IDKNQIQLFNLESSKIEVILKNAI
sp P10845 BXA1_CLOBO	ESNHLIDLRLRYASKINIGSKVNFDP-IDKNQIQLFNLESSKIEVILKNAI
tr Q2PPK6 Q2PPK6_CLOBO	KKDDLIDLRLRYGAKINIGDRVYYS-IDKNQIKLINLESSTIEVILKNAI
sp Q45894 BXA2_CLOBO	KKDDLIDLRLRYGAKINIGDRVYYS-IDKNQIKLINLESSTIEVILKNAI
tr Q3LRX8 Q3LRX8_CLOBO	KDDDLIDLRLRYGAEIYNGDKVYYNS-IDKNQIRLINLESSTIEVILKNAI :.: *.: *.: *.: *.: *.: *.: *.: *.: *.: *
sp P04958 TETX_CLOTE	EYNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISSMKKHSLSIGSGW
tr Q7B8V4 Q7B8V4_CLOBO	VYNSMYENFSTSFWRIPKYFN---SISLNNEYTIINCMENN-----SGW
sp P10845 BXA1_CLOBO	VYNSMYENFSTSFWRIPKYFN---SISLNNEYTIINCMENN-----SGW
tr Q2PPK6 Q2PPK6_CLOBO	VYNSMYENFSTSFWRIPKYFS---KINLNNEYTIINCIENN-----SGW
sp Q45894 BXA2_CLOBO	VYNSMYENFSTSFWRIPKYFS---KINLNNEYTIINCIENN-----SGW
tr Q3LRX8 Q3LRX8_CLOBO	VYNSMYENFSTSFWRIPKYFN---SISLNNEYTIINCMENN-----SGW * * :.: *.: *.: *.: *.: *.: *.: *.: *.: *.: *
sp P04958 TETX_CLOTE	SVSLKGNNLIWTLKDSAGEVRQITFRDLDPKFNAYLANKWVFITITNDRL
tr Q7B8V4 Q7B8V4_CLOBO	KVSLNYGEIIWTLQDTQEIKQRVVFYKYSQMINISDYINRWIFVTITNNRL
sp P10845 BXA1_CLOBO	KVSLNYGEIIWTLQDTQEIKQRVVFYKYSQMINISDYINRWIFVTITNNRL
tr Q2PPK6 Q2PPK6_CLOBO	KVSLNYGEIIWTLQDNKQNIQRVVFYKYSQMVNISDYINRWIFVTITNNRL
sp Q45894 BXA2_CLOBO	KVSLNYGEIIWTLQDNKQNIQRVVFYKYSQMVNISDYINRWIFVTITNNRL
tr Q3LRX8 Q3LRX8_CLOBO	KVSLNYGEIIWTFQDTQEIKQRVVFYKYSQMINISDYINRWIFVTITNNRI : * * :.: *.: *.: *.: *.: *.: *.: *.: *.: *.: *
sp P04958 TETX_CLOTE	SSANLYINGVLMGSAEITGLGAIREDDNNITLKLDRCNNNNQYVSIDKFRI
tr Q7B8V4 Q7B8V4_CLOBO	NNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIYFNL
sp P10845 BXA1_CLOBO	NNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIYFNL
tr Q2PPK6 Q2PPK6_CLOBO	TKSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDPRRYIMIKYFNL
sp Q45894 BXA2_CLOBO	TKSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDPRRYIMIKYFNL
tr Q3LRX8 Q3LRX8_CLOBO	TKSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDPRRYIVIKYFNL : * * :.: *.: *.: *.: *.: *.: *.: *.: *.: *.: *
sp P04958 TETX_CLOTE	FCKALNPKEIEKLYTSYLSITFLRDFWGNPLRYDTEYYLIPVASSSK--D

tr Q7B8V4 Q7B8V4_CLOBO	FDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKPYYMLNLYDPNKYVD
sp P10845 BXA1_CLOBO	FDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKPYYMLNLYDPNKYVD
tr Q2PPK6 Q2PPK6_CLOBO	FDKELNEKEIKDLYDSQSN SGILKDFWGNLYQYDKPYYMLNLFDPNKYVD
sp Q45894 BXA2_CLOBO	FDKELNEKEIKDLYDSQSN SGILKDFWGNLYQYDKPYYMLNLFDPNKYVD
tr Q3LRX8 Q3LRX8_CLOBO	FDKELSEKEIKDLYDNQSN SGILKDFWGDYLYQYDKSYMLNLYDPNKYVD
	* * * . ***: . ** . . :*:****: *:***. **: : ...* *
sp P04958 TETX_CLOTE	VQLKNITDYMILT NAPSYTNGKLN IYRRLYNGLKFIIKRYTPNNEIDSF
tr Q7B8V4 Q7B8V4_CLOBO	VNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGN-KDNI
sp P10845 BXA1_CLOBO	VNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGN-KDNI
tr Q2PPK6 Q2PPK6_CLOBO	VNNIGIRGYMYLKGPRGSVVT TNIYLNSTLYEGTKFIIKKYASGN-EDNI
sp Q45894 BXA2_CLOBO	VNNIGIRGYMYLKGPRGSVVT TNIYLNSTLYEGTKFIIKKYASGN-EDNI
tr Q3LRX8 Q3LRX8_CLOBO	VNNVGIRGYMYLKGPRDNVMTTNIYLNSSLYMGTKFIIKKYASGN-KDNI
	*: . * .****... . . . ** * *****:*.:. * ..:
sp P04958 TETX_CLOTE	VKSGDFIKLYVSYN NNEHIVGYPKDGN AFNNLDRILRVGYNAPGIPLYKK
tr Q7B8V4 Q7B8V4_CLOBO	VRNNDRVYINVVVK NKEYRLATNASQAGVEKILSALEIPDVGN--LSQVV
sp P10845 BXA1_CLOBO	VRNNDRVYINVVVK NKEYRLATNASQAGVEKILSALEIPDVGN--LSQVV
tr Q2PPK6 Q2PPK6_CLOBO	VRNNDRVYINVVVK NKEYRLATNASQAGVEKILSALEIPDVGN--LSQVV
sp Q45894 BXA2_CLOBO	VRNNDRVYINVVVK NKEYRLATNASQAGVEKILSALEIPDVGN--LSQVV
tr Q3LRX8 Q3LRX8_CLOBO	VRNNDRVYINVVVK NKEYRLATNASQAGVEKILSALEIPDVGN--LSQVV
	:.. : : * :*:*: :. . .: : *.: .
sp P04958 TETX_CLOTE	MEAVKLRLDKTYSVQLKLYDDKNASLGLVGTHNGQIGNDPNRDILIASNW
tr Q7B8V4 Q7B8V4_CLOBO	VMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNN-----IAKLVASNW
sp P10845 BXA1_CLOBO	VMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNN-----IAKLVASNW
tr Q2PPK6 Q2PPK6_CLOBO	VMKSKDDQGIRNKCKMNLQDNNGNDIGLIGFHQFNN-----IAKLVASNW
sp Q45894 BXA2_CLOBO	VMKSKDDQGIRNKCKMNLQDNNGNDIGFIGFHL YDN-----IAKLVASNW
tr Q3LRX8 Q3LRX8_CLOBO	VMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNN-----IAKLVASNW
	: * : . :*: **: . .:*: * * : *:****
sp P04958 TETX_CLOTE	YFNHLK--DKILGCDWYFVPTDEGWTND--
tr Q7B8V4 Q7B8V4_CLOBO	YNRQIERSSRTLGC SWEFIPVDDGWGERPL
sp P10845 BXA1_CLOBO	YNRQIERSSRTLGC SWEFIPVDDGWGERPL
tr Q2PPK6 Q2PPK6_CLOBO	YNRQVGKASRTFGC SWEFIPVDDGWGESSL
sp Q45894 BXA2_CLOBO	YNRQVGKASRTFGC SWEFIPVDDGWGESSL
tr Q3LRX8 Q3LRX8_CLOBO	YNRQIERSSRTLGC SWEFIPVDDGWRERPL
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